**AMENDMENTS TO THE SPECIFICATION**:

Please replace the paragraph starting on page 7, line 2 with the following paragraph:

The present invention encompasses nucleic acid molecules which are complementary to the nucleotide sequence of miRNA listed in the above table 1. Moreover, a nucleotide sequence which has an identity of at least 80%, preferably of at least 90% and more preferably of at least 95%, to the nucleotide sequence selected from the group of consisting of SEQ ID NOs: 1-17 or the complementary sequence thereof, is included in the present invention. The term "identity" refers to the degree of sequence identity between two nucleic acid sequences, more particularly to the degree that two bases on the same position precisely corresponds to each other in two aligned sequences. The identity can be determined using a identity search program known in the pertinent art such as BLAST ~~(http://www.ncbi.nlm.nih.gov/BLAST/)~~, FASTA ~~(http://bioweb.pasteur.fr/seqanal/interfaces/fasta.html)~~ or Smith Waterman Algorithm etc.

Please replace the paragraph starting on page 9, line 3 with the following:

The miRNA precursor molecules may be identified using known methods in the pertinent art, such as, MFOLD program ~~(http://www.bioinfo.rpi.edu/applications/mfold/old/rna)~~ (Zuker *et al.*, Algorithms and Thermodynamics for RNA Secondary Structure Prediction: A Practical Guide. Kluwer Academic Publishing, Dordrecht, The Netherlands, 1999).

Please replace the paragraph starting on page 25, line 21 with the following:

MiRNAs were cloned from the cDNA libraries constructed in the Example <1-1> using the method of Lagos-Quintana et al. (Lagos-Quintana *et al.*, *Science*, 294: 853-858, 2001). Database searches of the cloned miRNAs were performed at the BLAST server ~~(http://www.ncbi.nlm.nih.gov/BLAST/)~~ (Altschul *et al.*, *J. Mol. Biol.* 215:403-410, 1990) and ENSEMBL server ~~(http://www.ensembl.org)~~ (Hubbard *et al.*, *Nucleic Acids Res.*, 30:38-41, 2002). Sequence alignment between miRNA sequences were performed by using CLUSTALW ~~(http://www.ebi.ac.uk/clustalw/)~~ (Higgins and Sharp, *Dev. Cell*, 5:351-358, 1988).

Please replace the paragraph starting on page 26, line 8, with the following:

To distinguish miRNAs from degradation products or small interfering RNAs (siRNAs), the present inventors evaluated the ability of RNA containing the clones to fold into stem-loop, that is, the secondary structure of the RNA by using the MFOLD program ~~(http://www.bioinfo.rpi.edu/applications/mfold/old/rna)~~ (Zuker *et al.*, Algorithms and Thermodynamics for RNA Secondary Structure Prediction: A Practical Guide. Kluwer Academic Publishing, Dordrecht, The Netherlands, 1999). Thirty-six RNAs were found in the stems of strong hairpin structures (see below Table 1 and Fig. 1).